


Exhibit 2

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View of

Swiss-Prot:

P26504

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Entry information

Entry name	LIPA_PSEFL
Primary accession number	P26504
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 23, August 1992
Sequence was last modified in	Release 23, August 1992
Annotations were last modified in	Release 46, February 2005
Name and origin of the protein	
Protein name	Lipase [Precursor]
Synonyms	EC 3.1.1.3 Triacylglycerol lipase
Gene name	None
From	Pseudomonas fluorescens [TaxID: 294]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

References

[1] NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

STRAIN=SIK W1;

MEDLINE=92118329;PubMed=1368740 [NCBI, ExPASy, EBI, Israel, Japan]

Chung G.H., Lee Y.P., Jeohn G.H., Yoo O.J., Rhee J.S.;

"Cloning and nucleotide sequence of thermostable lipase gene from Pseudomonas fluorescens SIK W1.";

Agric. Biol. Chem. 55:2359-2365(1991).

Comments

- **CATALYTIC ACTIVITY:** Triacylglycerol + H₂O = diacylglycerol + a carboxylate.
- **BIOPHYSICOCHEMICAL PROPERTIES:**
Temperature dependence Thermostable;
- **SIMILARITY:** Belongs to the AB hydrolase superfamily. Lipase family.

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Cross-references

EMBL S77830; AAC60402.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
D11455; BAA02012.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]

PIR JQ1277; JQ1277.
IPR001343; Hemlysn_Ca_bind.
IPR002921; Lipase_3.

InterPro IPR008262; Lipase_AS.
IPR009006; Racem_decarbox_C.
Graphical view of domain structure.
PF00353; HemolysinCabind; 2.

Pfam PF01764; Lipase_3; 1.
Pfam graphical view of domain structure.

PRINTS PR00313; CABNDNGRPT.

PROSITE PS00330; HEMOLYSIN_CALCIIUM; 1.
PS00120; LIPASE_SER; 1.

ProDom [Domain structure / List of seq. sharing at least 1 domain]

HOBACGEN [Family / Alignment / Tree]

BLOCKS P26504.

ProtoNet P26504.

ProtoMap P26504.

PRESAGE P26504.

DIP P26504.

ModBase P26504.

SMR P26504; 16E539323D5D0DD8.

SWISS-2DPAGE Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Direct protein sequencing; Hydrolase; Lipid degradation; Signal.

Features



Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	23	23	Potential.
CHAIN	24	449	426	Lipase.
ACT_SITE	206	206		Charge relay system (By similarity).

Sequence information

Length: 449 AA [This is the length of the unprocessed precursor] Molecular weight: 48233 Da [This is the MW of the unprocessed precursor] CRC64: 16E539323D5D0DD8 [This is a checksum on the sequence]

```

      10      20      30      40      50      60
MGVFDYKNLG TEASKTLFAD ATAITLYTYH NLDNGFAVGY QQHGLGLGCR HTGRGVARQH

      70      80      90     100     110     120
RLPGSDPPAF PGILTRKRFP WTRCTQPVGR QSSASALGYG GKVDARGTFF GEKAGYTAAQ

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      130      140      150      160      170      180
AEVLGKYDDA GKLEIGIGF RGTSGPRESL ITTPCRSGQR PARRAGPQGL CEKLCRRTFG

      190      200      210      220      230      240
GLLKTVADYA GAHGLSGKDV LVSGHSLGGL AVNSMADLST SKWAGFYKDA NYLAYASPTQ

      250      260      270      280      290      300
SAGDKVLNIG YENDPVFRAI DGSTFNLSSL GVHDKAHEST TDNIVSFNDH YASTLWNVLP

      310      320      330      340      350      360
FSIANLSTWV SHLPSAYGDG MTRVLESGFY EQMTRDSTII LCPTWSDPAR ANTWVQDLNR

      370      380      390      400      410      420
NAEPHTGNTF IIGSDGNDLI QGGKGADFIE GKGKNDTIRD NSGHNTFLFS GHFGQDRIIG

      430      440
YQPTGWCSRA PTAAPTCATT RRPWGPIRC

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P26504 in FASTA
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BLAST submission on
BLAST ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



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